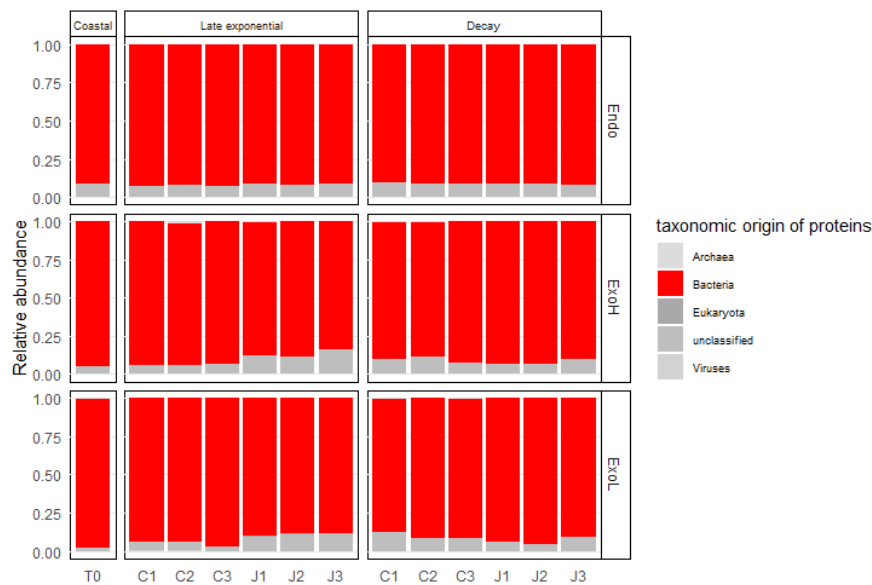


Additional file 3 to Tinta et al. Jellyfish detritus supports niche partitioning and metabolic interactions among marine bacteria

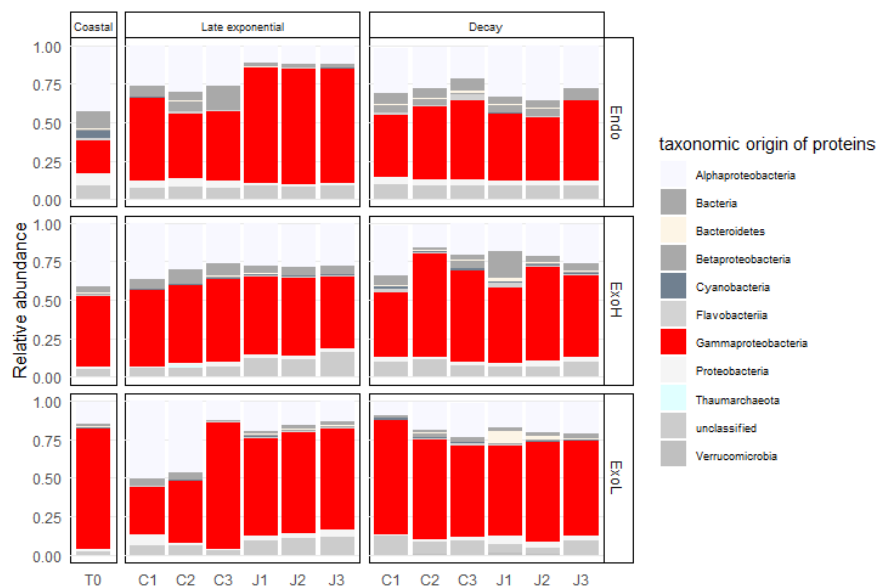
Supplementary Figures

Figure S1: Taxonomic origin of proteins at **A)** superkingdom, **B)** class, **C)** order and **D)** family level. Higher taxonomic level was assigned when taxa could not be classified down to class/order/family level. Note: in y axes 1 equals 100%.

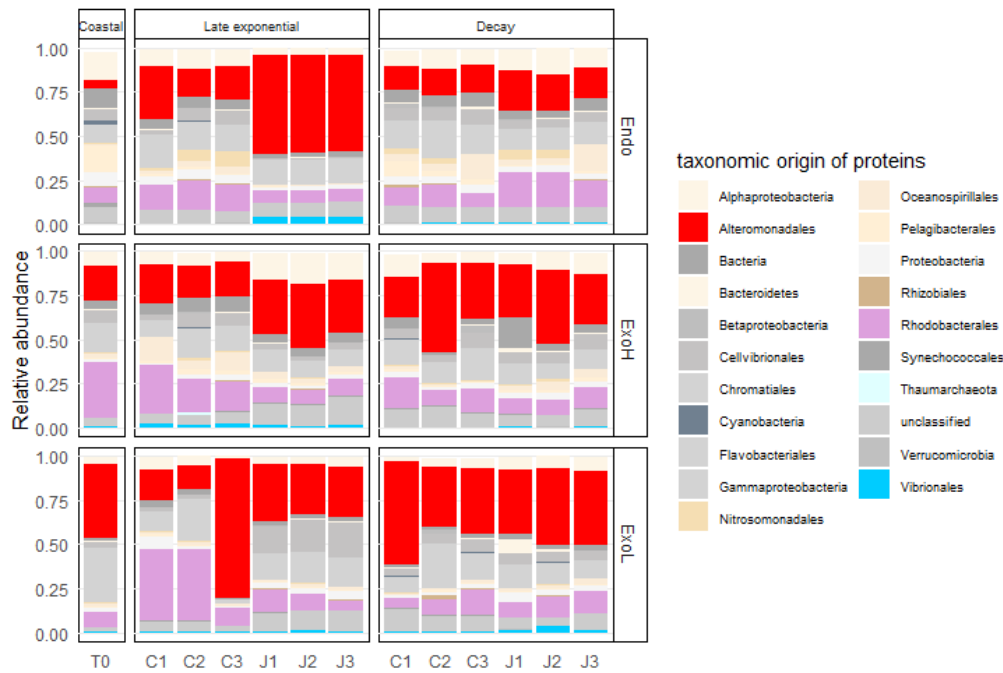
A. Superkingdom



B. Class



C. Order



D. Family

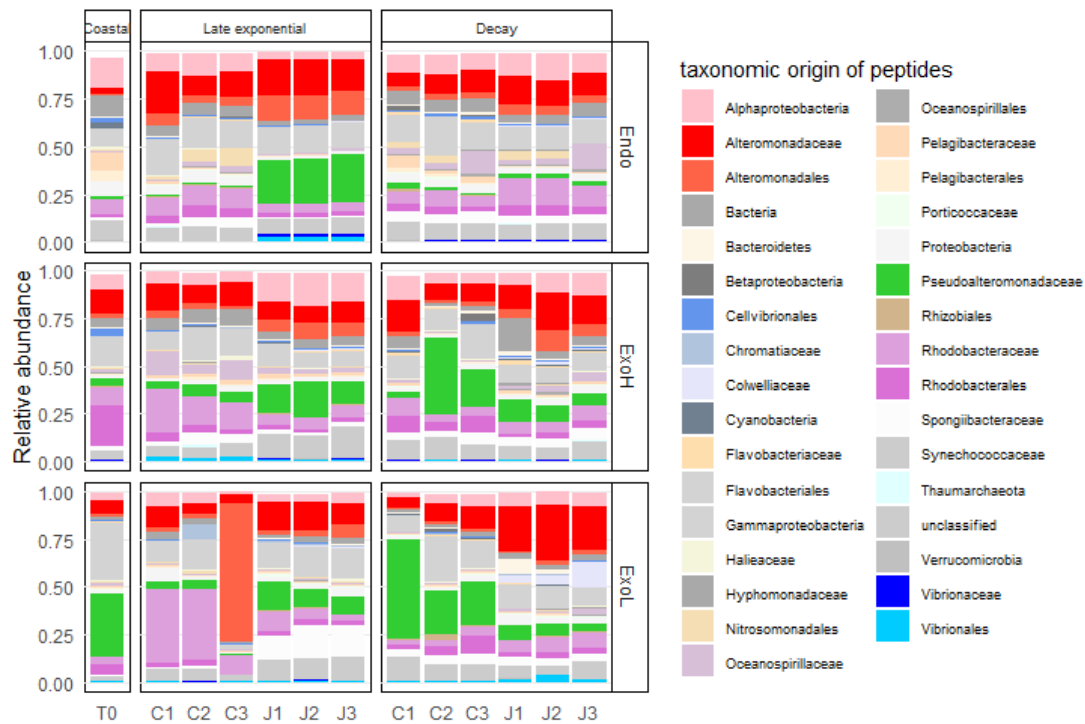
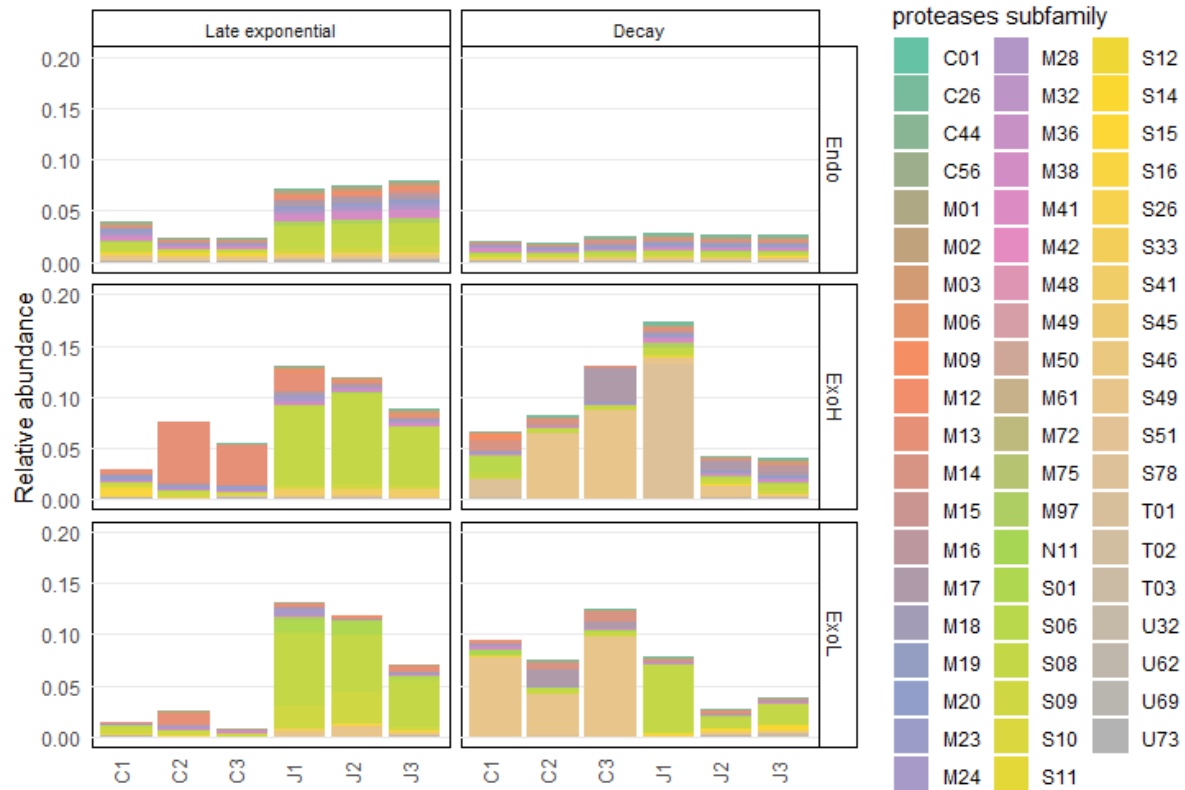
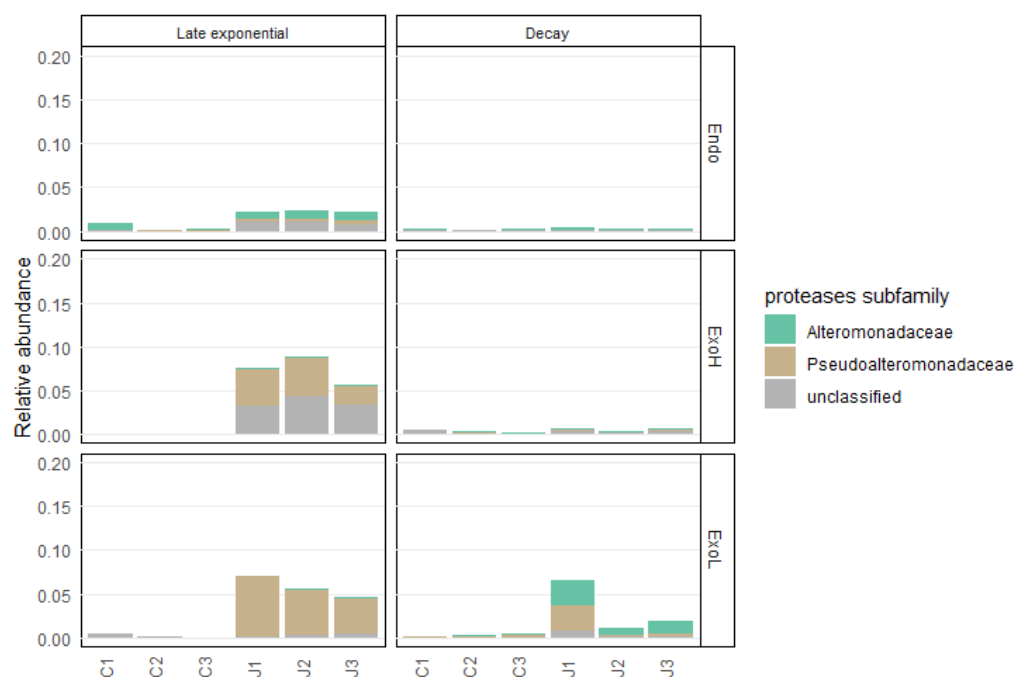


Figure S2: Relative abundance of protease (A) and CAZyme (B) subfamilies significantly enriched in meta- and exo-proteomes from jelly-OM as compared to control treatments. Note: in y-axes 1 equals 100%.

A.1 Subfamilies of protease. C – cysteine peptidase, M – metallo peptidase, N – asparagine peptidase, S – serine peptidase, T – threonine peptidases, U – unknown. Consecutive number is subfamily identifier.



A.2 Taxonomic origin of S08 subfamily



A.3 Taxonomic origin of M9A subfamily

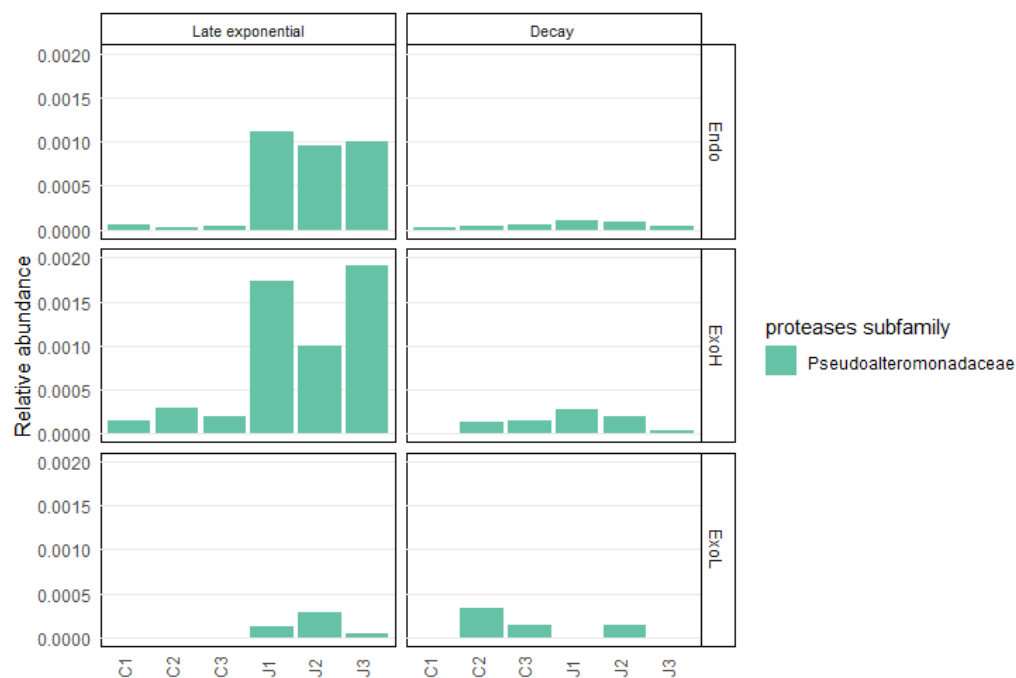
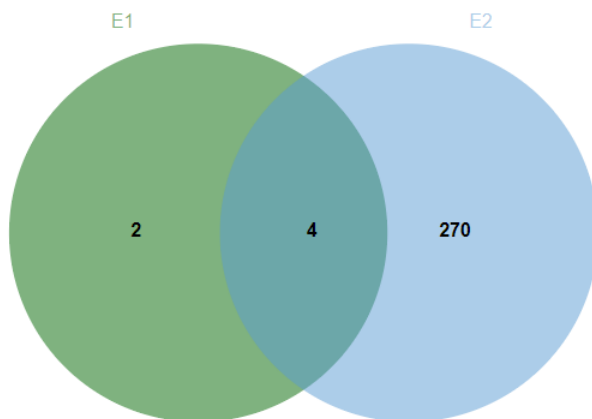
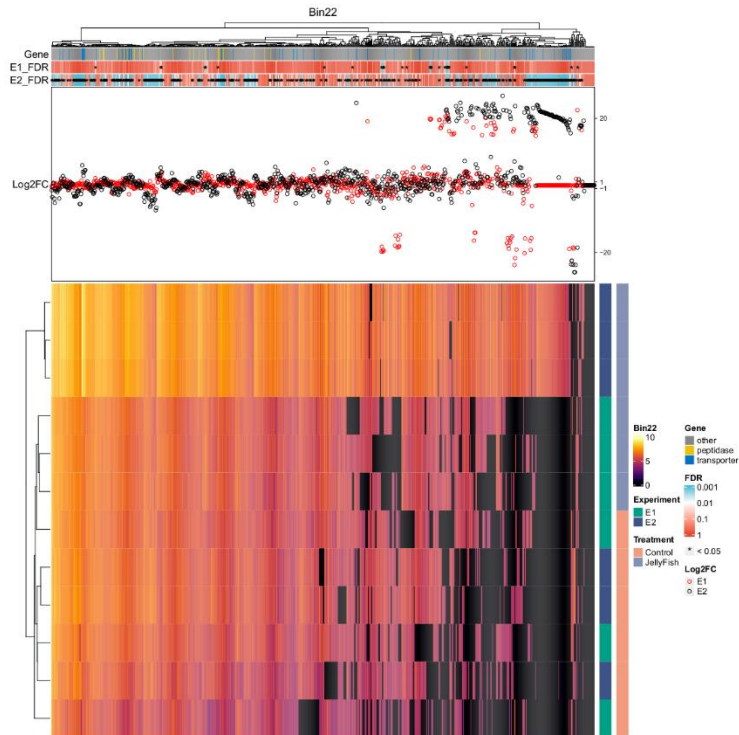
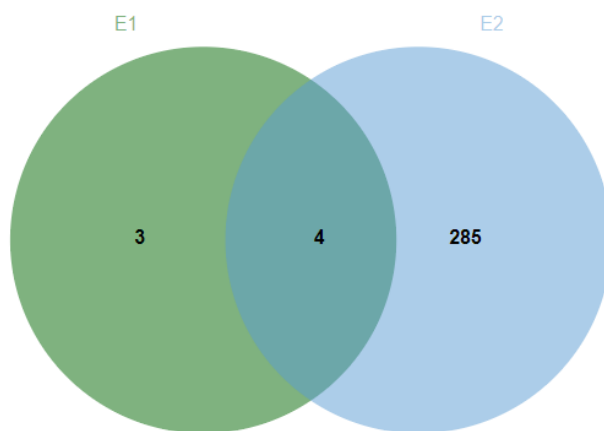
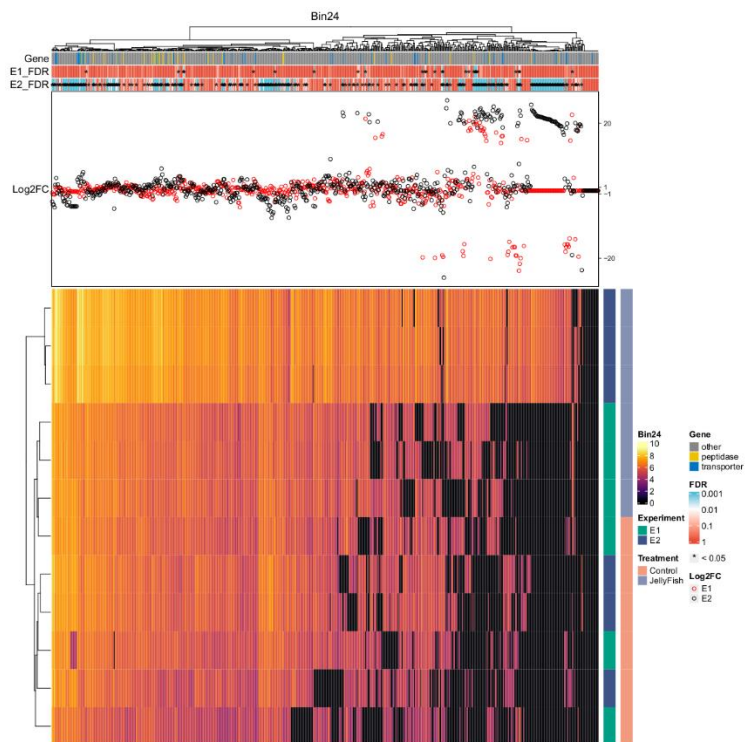


Figure S3: A. Supplementary to Figure 4: High-resolution heatmaps and Venn diagrams of differentially abundant proteins for each key MAG during different stages of the jelly-OM degradation process.

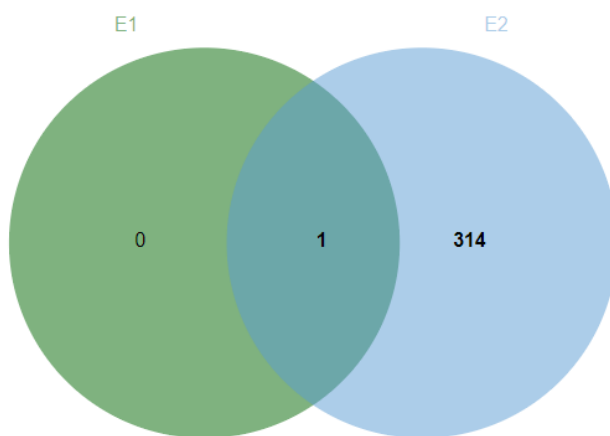
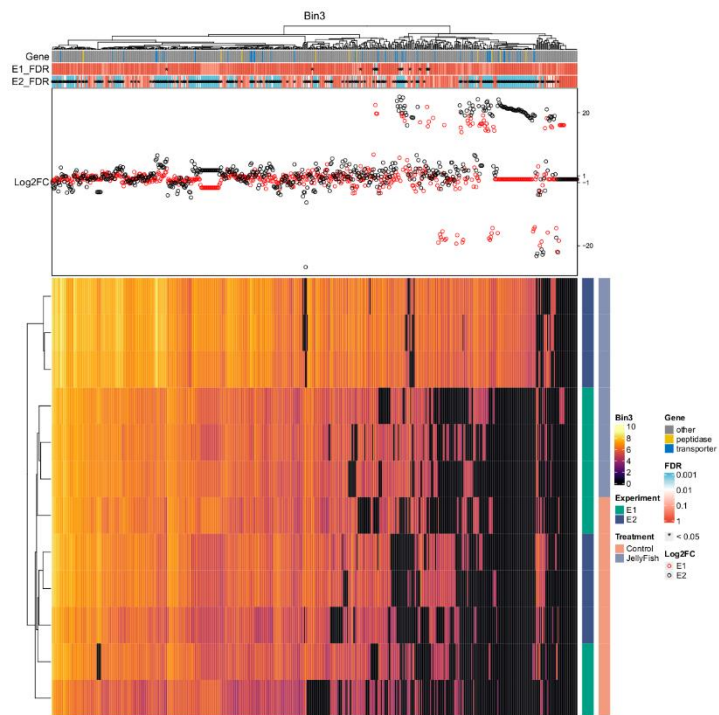
Pseudoalteromonas MAG 22



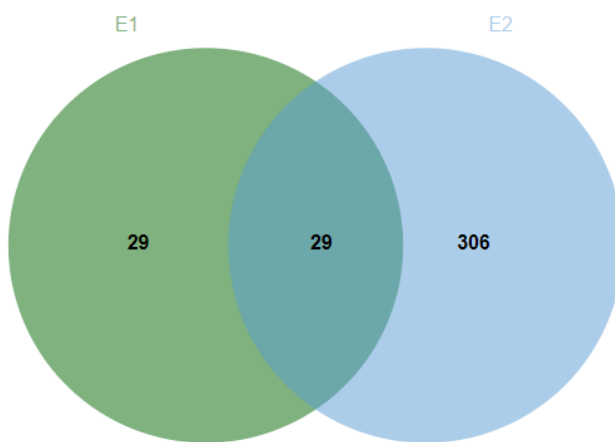
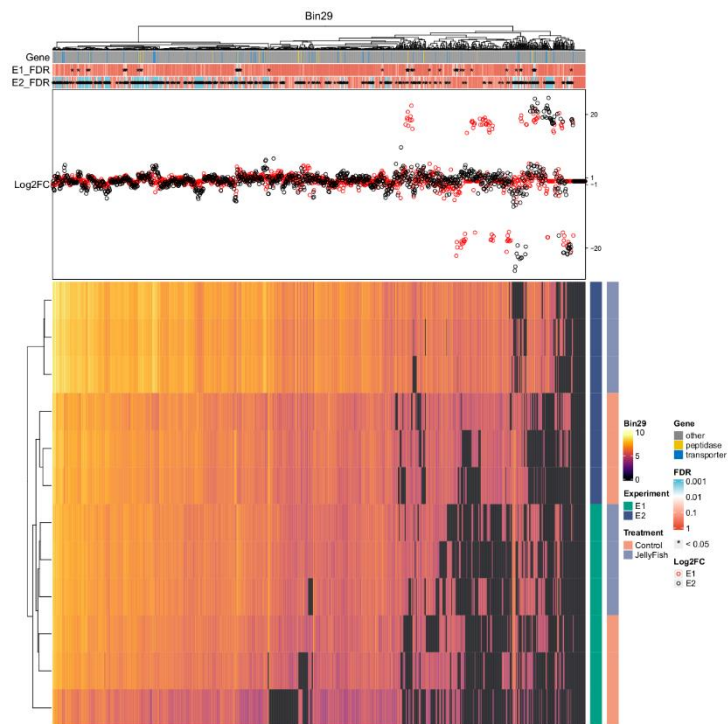
Pseudoalteromonas MAG 24



Vibrio MAG 3



Alteromonas MAG 29



Thalassobius MAG 51

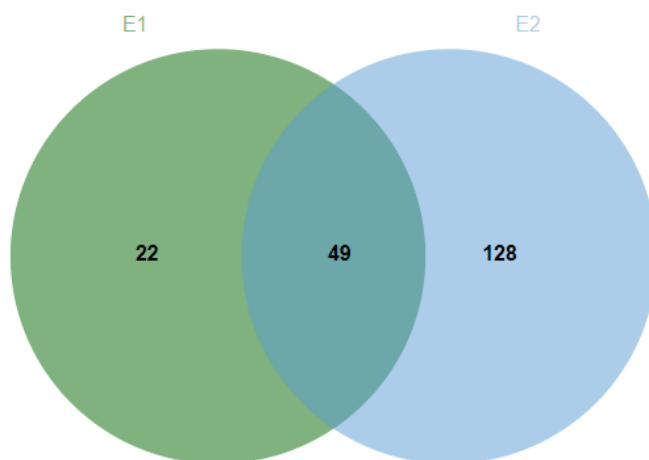
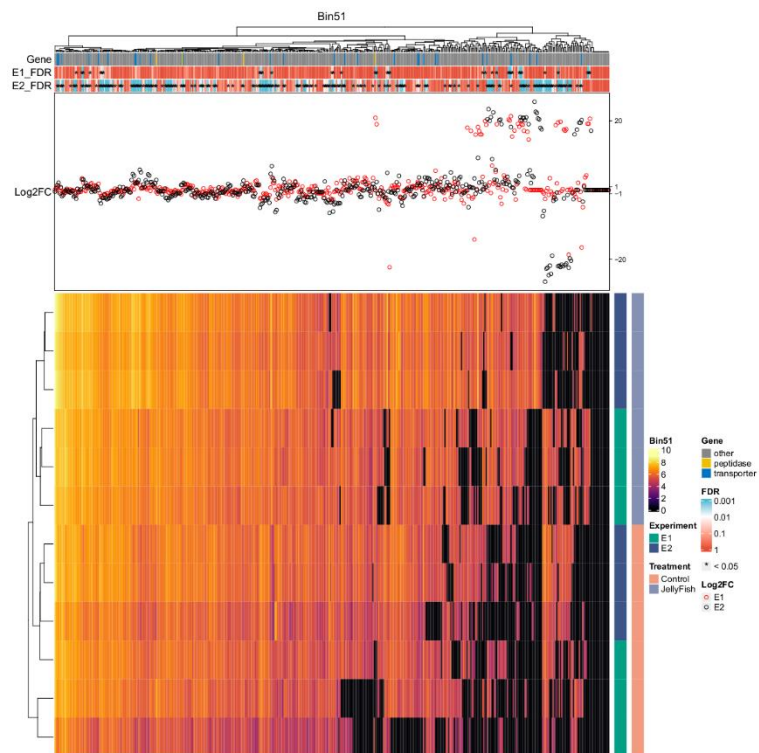
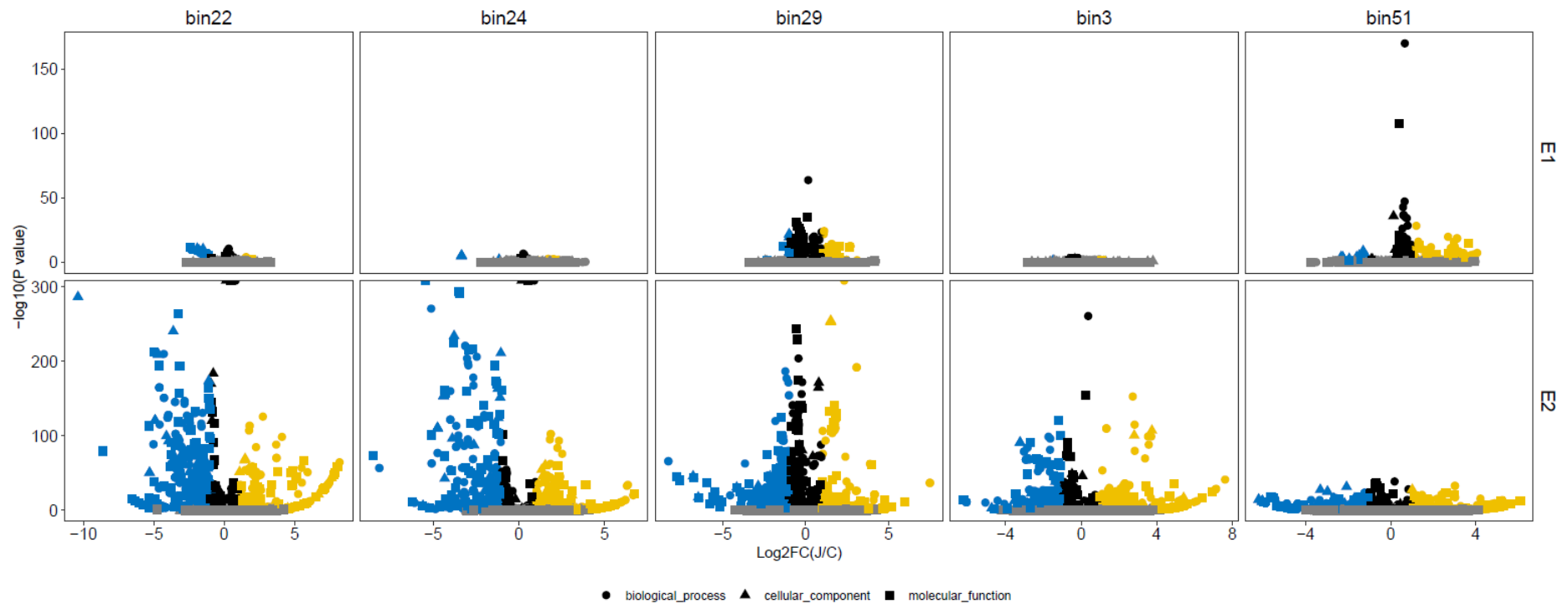


Figure S4: A.) GO-annotated and **B.)** KEGG-annotated differentially abundant proteins (enrichment as log2FC and significance as p-value or FDR) per each MAG during different stage of jelly-OM degradation process. *Pseudoalteromonas*: bin22 and bin24; *Alteromonas*: bin29; *Vibrio*: bin3; *Thalassobius*: bin51. Circles: proteins related to biological processes, Triangles: proteins related to cellular components, Squares: proteins related to molecular function. Blue: proteins up-regulated in jelly-OM (as compared to control) treatments. Yellow: proteins down-regulated in jelly-OM (as compared to control) treatments. Grey: proteins with no significant difference in expression between jelly-OM and control treatments. E2: late exponential growth phase of jelly-OM degrading community; E1: decay phase of jelly-OM degrading community

A.



B.

